GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:11:54 ; Search time 36808 Seconds
(without alignments)
1366.270 Million cell updates/sec

Title: US-09-920-394-3_COPY_14_1741
Perfect score: 1728
Sequence: 1 tgtcgcccttcacgatgtgg.....catagagctgtgaatgaaga 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	40	2.3	40	6	AX092543	AX092543 Sequence
c	2	35.2	2.0	40	6	AX092544	AX092544 Sequence
c	3	25	1.4	25	6	AX092546	AX092546 Sequence
	4	21.2	1.2	35	6	AR153460	AR153460 Sequence
c	5	20.8	1.2	48	6	AX229460	AX229460 Sequence
c	6	20.6	1.2	35	6	AR022645	AR022645 Sequence
c	7	20.6	1.2	35	6	AR150983	AR150983 Sequence
c	8	20.6	1.2	35	6	AR156053	AR156053 Sequence
c	9	20.6	1.2	35	6	AX029519	AX029519 Sequence
c	10	20.6	1.2	35	6	I87993	I87993 Sequence 3
c	11	20.6	1.2	47	6	AX194737	AX194737 Sequence
	12	20.4	1.2	32	6	A76878	A76878 Sequence 10
c	13	20.4	1.2	48	6	AX229366	AX229366 Sequence
c	14	20.4	1.2	50	9	HUMKEREP8	L00204 Human K6b (
c	15	20.2	1.2	30	6	AR068140	AR068140 Sequence
c	16	20.2	1.2	30	6	I31742	I31742 Sequence 6
c	17	20.2	1.2	30	6	I33417	I33417 Sequence 6
c	18	20.2	1.2	30	6	I38169	I38169 Sequence 6
c	19	20.2	1.2	30	6	I51133	I51133 Sequence 6
	20	20.2	1.2	40	6	A05823	A05823 Oligonucleo
c	21	20.2	1.2	43	9	HSU30421	U30421 Human isola
	22	20	1.2	31	6	AX463826	AX463826 Sequence
c	23	19.6	1.1	50	9	HSAJ4655	AJ224655 Homo sapi
c	24	19.4	1.1	39	6	AR116809	AR116809 Sequence
c	25	19.4	1.1	47	6	I68603	I68603 Sequence 3
c	26	19.4	1.1	48	6	E02389	E02389 DNA probe f
	27	19.4	1.1	49	6	AX342584	AX342584 Sequence
	28	19.2	1.1	39	6	A93638	A93638 Sequence 8
	29	19.2	1.1	39	6	AX023201	AX023201 Sequence
	30	19.2	1.1	40	10	MUSTRBRK	L35090 Mus musculu
c	31	19.2	1.1	43	6	AR028659	AR028659 Sequence
c	32	19.2	1.1	43	6	AR053752	AR053752 Sequence
c	33	19.2	1.1	43	6	AR146252	AR146252 Sequence
c	34	19.2	1.1	43	6	AR178206	AR178206 Sequence
c	35	19.2	1.1	43	6	I73331	I73331 Sequence 27
c	36	19.2	1.1	48	6	AX426723	AX426723 Sequence
	37	19.2	1.1	49	6	A05822	A05822 Oligonucleo
	38	19.2	1.1	49	6	AR009419	AR009419 Sequence
c	39	19.2	1.1	49	6	AR009443	AR009443 Sequence
	40	19.2	1.1	49	6	AR009444	AR009444 Sequence
c	41	19.2	1.1	49	6	AX167829	AX167829 Sequence
	42	19.2	1.1	49	6	AX167830	AX167830 Sequence
	43	19.2	1.1	49	6	I16524	I16524 Sequence 3
c	44	19.2	1.1	49	6	I16548	I16548 Sequence 28
	45	19.2	1.1	49	6	I16549	I16549 Sequence 29

ALIGNMENTS

RESULT 1
AX092543
LOCUS AX092543 40 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 4 from Patent WO0116358.
ACCESSION AX092543
VERSION AX092543.1 GI:13444635
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 40)
AUTHORS Borg-Capra,C.S., Lehner,R.J. and Vance,D.E.
TITLE Method of screening for triacyglycerol hydrolase inhibitors
JOURNAL Patent: WO 0116358-A 4 08-MAR-2001;
GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF

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            ALBERTA (CA)
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligo"
BASE COUNT       10 a      10 c      13 g       7 t
ORIGIN

  Query Match             2.3%;  Score 40;  DB 6;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     535 GCATCTGGGGATTCTTCAGCACAGGGGATGAACACAGCCG 574
           ||||||||||||||||||||||||||||||||||||||||
Db       1 GCATCTGGGGATTCTTCAGCACAGGGGATGAACACAGCCG 40


RESULT 2
AX092544/c
LOCUS       AX092544                 40 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 5 from Patent WO0116358.
ACCESSION   AX092544
VERSION     AX092544.1  GI:13444636
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Borg-Capra,C.S., Lehner,R.J. and Vance,D.E.
  TITLE     Method of screening for triacyglycerol hydrolase inhibitors
  JOURNAL   Patent: WO 0116358-A 5 08-MAR-2001;
            GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF
            ALBERTA (CA)
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligo"
BASE COUNT       10 a      9 c       9 g      12 t
ORIGIN

  Query Match             2.0%;  Score 35.2;  DB 6;  Length 40;
  Best Local Similarity   92.5%;  Pred. No. 95;
  Matches   37;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1491 CTTAGCAAGATGGTGATGAAATTCTGGGCCAACTTTGCTC 1530
           || ||||| |||||||||||||| ||||||||||||||||
Db      40 CTCAGCAAAATGGTGATGAAATACTGGGCCAACTTTGCTC 1


RESULT 3
AX092546/c
LOCUS       AX092546                 25 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 7 from Patent WO0116358.
ACCESSION   AX092546
VERSION     AX092546.1  GI:13444638
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Borg-Capra,C.S., Lehner,R.J. and Vance,D.E.
  TITLE     Method of screening for triacyglycerol hydrolase inhibitors
  JOURNAL   Patent: WO 0116358-A 7 08-MAR-2001;
            GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF
            ALBERTA (CA)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligo"
BASE COUNT        3 a       6 c       6 g      10 t
ORIGIN

  Query Match             1.4%;  Score 25;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1697 CCAGACAGAACACATAGAGCTGTGA 1721
           |||||||||||||||||||||||||
Db      25 CCAGACAGAACACATAGAGCTGTGA 1


RESULT 4
AR153460
LOCUS       AR153460                 35 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 30 from patent US 6235515.
ACCESSION   AR153460
VERSION     AR153460.1  GI:15120992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
            Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
            Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
  TITLE     Malathion carboxylesterase
  JOURNAL   Patent: US 6235515-A 30 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        4 a       8 c       7 g       5 t      11 others
ORIGIN

  Query Match             1.2%;  Score 21.2;  DB 6;  Length 35;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches   21;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     165 TTCCTGGGAATCCCTTTGCCAAGCCGCCTCTTGG 199
           |||. ||| || || | :|| :|:|| || :| ||
Db       1 TTCGAGGGNATNCCNTAYGCNMARCCNCCNBTNGG 35


RESULT 5
AX229460/c
LOCUS       AX229460                 48 bp    mRNA    linear   PAT 10-SEP-2001
DEFINITION  Sequence 2832 from Patent WO0157206.
ACCESSION   AX229460
VERSION     AX229460.1  GI:15558601
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 2832 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       10 a      10 c      14 g      14 t
ORIGIN

  Query Match             1.2%;  Score 20.8;  DB 6;  Length 48;
  Best Local Similarity   64.6%;  Pred. No. 1.4e+06;
  Matches   31;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy     963 CAACCCCTTCTGGGCACTGTGATTGATGGGATGCTGCTGCTGAAAACA 1010
           |||||| | | || |  |||  |||| ||||    | || |  |||| |
Db      48 CAACCCTTCCCGGACGATGTCCTTGAAGGGAGTTTCCTCCGAAAAAAA 1
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RESULT 6
AR022645/c
LOCUS       AR022645                35 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5792931.
ACCESSION   AR022645
VERSION     AR022645.1  GI:3976707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Duvick,J., Rood,T., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 5792931-A 3 11-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        5 a      6 c      7 g      6 t     11 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 1.6e+06;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 7
AR150983/c
LOCUS       AR150983                35 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6229071.
ACCESSION   AR150983
VERSION     AR150983.1  GI:15115574
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6229071-A 3 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        5 a      6 c      7 g      6 t     11 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 1.6e+06;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 8
AR156053/c
LOCUS       AR156053                35 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6239330.
ACCESSION   AR156053
VERSION     AR156053.1  GI:15124106
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Duvick,J., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6239330-A 3 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        5 a      6 c      7 g      6 t     11 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 1.6e+06;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 9
AX029519/c
LOCUS       AX029519                35 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 3 from Patent EP0981953.
ACCESSION   AX029519
VERSION     AX029519.1  GI:10190256
KEYWORDS    .
SOURCE      Exophiala spinifera.
  ORGANISM  Exophiala spinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;
            Chaetothyriales; Herpotrichiellaceae; mitosporic
            Herpotrichiellaceae; Exophiala.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Transgenic plants transformed with fumonisin detoxifying enzymes
  JOURNAL   Patent: EP 0981953-A 3 01-MAR-2000;
            PIONEER HI BRED INT (US)
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Exophiala spinifera"
                     /db_xref="taxon:91928"
BASE COUNT        5 a      6 c      7 g      6 t     11 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 1.6e+06;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 10
I87993/c
LOCUS       I87993                  35 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 3 from patent US 5716820.
ACCESSION   I87993
VERSION     I87993.1  GI:3407933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Duvick,J., Rood,T. and Wang,X.
  TITLE     Fumonisin detoxification enzymes
  JOURNAL   Patent: US 5716820-A 3 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT        5 a      6 c      7 g      6 t     11 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 1.6e+06;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
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          ||:||:|| :  ||:|| || :|:||| |||
Db     35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5
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RESULT 11
AX194737/c
LOCUS       AX194737                47 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 207 from Patent WO0151659.
ACCESSION   AX194737
VERSION     AX194737.1  GI:15385384
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Chu,T., Blumenfeld,M. and Cohen,D.
  TITLE     Biallelic markers derived from genomic regions carrying genes
            involved in central nervous system disorders
  JOURNAL   Patent: WO 0151659-A 207 19-JUL-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       24
                     /note="18-289-239 : polymorphic base C or T"
BASE COUNT       12 a     14 c      3 g     17 t      1 others
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 6;  Length 47;
  Best Local Similarity   70.3%;  Pred. No. 1.6e+06;
  Matches   26;  Conservative    1;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    672 GGAGAGTCAGCGGGAGGAGAAAGTGTCTCTGTTCTTG 708
          ||||||  |||   ||:||||| ||||| |||  | |
Db     40 GGAGAGGTAGCAATAGRAGAAAATGTCTTTGTAATAG 4


RESULT 12
A76878
LOCUS       A76878                  32 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 10 from Patent WO9315198.
ACCESSION   A76878
VERSION     A76878.1  GI:6088683
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Denefle,P. and Guinet,F.
  TITLE     POLYPEPTIDES DERIVED FROM HUMAN AIV APOLIPOPROTEIN, PREPARATION AND
            USE THEREOF
  JOURNAL   Patent: WO 9315198-A 10 05-AUG-1993;
            RHONE POULENC RORER SA (FR)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a      5 c     12 g      9 t
ORIGIN

  Query Match             1.2%;  Score 20.4;  DB 6;  Length 32;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+06;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    411 AGGCTGCCGGTGATGGTGTGGATCCACGGA 440
          | | ||  |||||||||| |||||||| |
Db      2 ATGGTGATGGTGATGGTGCGGATCCACGCA 31


RESULT 13
AX229366/c
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LOCUS       AX229366                48 bp    mRNA    linear   PAT 10-SEP-2001
DEFINITION  Sequence 2738 from Patent WO0157206.
ACCESSION   AX229366
VERSION     AX229366.1  GI:15558507
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 2738 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        9 a     14 c     14 g     11 t
ORIGIN

  Query Match             1.2%;  Score 20.4;  DB 6;  Length 48;
  Best Local Similarity   65.2%;  Pred. No. 1.9e+06;
  Matches   30;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    963 CAACCCCTTCTGGGCACTGTGATTGATGGGATGCTGCTGCTGAAAA 1008
          ||| |||| | || |  |||  |||| ||||   | || | || ||
Db     48 CAAACCCTCCCGGACGATGTCCTTGAAGGGAGTTTCCTCCGGAGAA 3


RESULT 14
HUMKEREP8/c
LOCUS       HUMKEREP8               50 bp    DNA     linear   PRI 08-JAN-1995
DEFINITION  Human K6b (epidermal keratin, type II) gene, exon 8.
ACCESSION   L00204
VERSION     L00204.1  GI:186713
KEYWORDS    keratin.
SEGMENT     8 of 9
SOURCE      Human DNA, clone GK-2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Tyner,A.L., Eichman,M.J. and Fuchs,E.
  TITLE     The sequence of a type II keratin gene expressed in human skin:
            conservation of structure among all intermediate filament genes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 82 (14), 4683-4687 (1985)
  MEDLINE   85270392
   PUBMED   2410904
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="12q11-q13"
     intron          <1. .13
                     /gene="KRTL1"
                     /note="K6b intron G"
     exon            14. .48
                     /gene="KRTL1"
                     /note="G00-120-132"
                     /number=8
     intron          49. .>50
                     /gene="KRTL1"
                     /note="K6b intron H"
BASE COUNT       12 a     13 c     13 g     12 t
ORIGIN      Undetermined number of bp after segment 7.

  Query Match             1.2%;  Score 20.4;  DB 9;  Length 50;
  Best Local Similarity   65.2%;  Pred. No. 1.9e+06;
  Matches   30;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1646 AGTAGCTTTCTGGACCAACCTCTTTGCCAAGAAGGCAGTGGAGAAG 1691
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Db     48 AGATGTTGACTTGTCCAACGCCTTCGCCATTCAGCCTGTGGAGAGG 3


RESULT 15
AR068140/c
LOCUS       AR068140                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5852187.
ACCESSION   AR068140
VERSION     AR068140.1  GI:5999362
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Thorner,M.O., Gaylinn,B.D., Horikawa,R. and Lyons,C.E. Jr.
  TITLE     Molecular cloning of the ovine pituitary growth hormone releasing
            hormone receptor
  JOURNAL   Patent: US 5852187-A 6 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        7 a     10 c     10 g      3 t
ORIGIN

  Query Match             1.2%;  Score 20.2;  DB 6;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 2e+06;
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Qy    599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
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Db     30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


Search completed: May 21, 2003, 05:36:39
Job time : 36831 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:09:54 ; Search time 392 Seconds
(without alignments)
9927.176 Million cell updates/sec

Title: US-09-920-394-3_COPY_14_1741
Perfect score: 1728
Sequence: 1 tgtcgcccttcacgatgtgg.....catagagctgtgaatgaaga 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	40	2.3	40	22	AAF75811	Triacylglycerol hy
c	2	39	2.3	50	22	AAL33656	Human SNP oligonuc
c	3	35.2	2.0	40	22	AAF75812	Triacylglycerol hy
	4	30	1.7	30	24	ABT04547	Human CES1 gene pr
c	5	25	1.4	25	22	AAF75814	Triacylglycerol hy
c	6	22.4	1.3	50	20	AAZ34198	Human PRO237 hybri
c	7	22.4	1.3	50	21	AAC78815	Human PRO237 hybri
c	8	22.4	1.3	50	21	AAC58128	Human PRO237 hybri
c	9	22.4	1.3	50	21	AAA88445	Antitumour PRO237
c	10	22.2	1.3	47	21	AAZ66351	Human map-related
	11	22	1.3	22	24	ABT04612	Human CES1 gene pr
	12	21.2	1.2	35	18	AAT68598	Md-alpha-E7 gene p
c	13	21.2	1.2	41	24	ABL52742	Nucleophosmin 9.68
c	14	21.2	1.2	41	24	ABL52743	Nucleophosmin 9.68
c	15	21	1.2	21	24	ABT04613	Human CES1 gene pr
	16	20.8	1.2	40	21	AAA51139	Oligomer sLT-A Rev
c	17	20.8	1.2	48	22	AAH97618	Human Chk1 ribozym
c	18	20.6	1.2	35	17	AAT13972	E. spinifera fumon
c	19	20.6	1.2	35	20	AAX05722	E. spinifera fumon
	20	20.6	1.2	47	21	AAZ67344	Human map-related
c	21	20.6	1.2	47	23	AAH88367	CNS disorder-relat
c	22	20.4	1.2	41	24	ABK15231	Geminivirus motion
c	23	20.4	1.2	48	22	AAH97524	Human Chk1 ribozym
	24	20.2	1.2	29	19	AAV58768	Human secreted pro
c	25	20.2	1.2	30	15	AAQ45309	Human acromegalic
c	26	20.2	1.2	30	18	AAT47106	Human acromegalic
c	27	20.2	1.2	30	20	AAV81455	Probe #2 for human
c	28	20.2	1.2	44	21	AAZ55430	Neisseria species
c	29	20.2	1.2	49	22	AAH25471	5' PCR primer used
	30	20	1.2	31	24	AAL47965	Recombinant porcin
c	31	20	1.2	45	20	AAX27669	[SPP]n internal re
c	32	20	1.2	45	24	ABL51767	Hydroxyproline-ric
c	33	20	1.2	47	21	AAA63889	Primer for cDNA en
	34	20	1.2	50	21	AAC27036	Human secreted pro
	35	19.8	1.1	42	18	AAT85655	Canine immunoglobi
	36	19.6	1.1	48	24	ABN72300	Streptococcus agal
	37	19.6	1.1	48	24	ABN72301	Streptococcus agal
c	38	19.6	1.1	50	21	AAA77273	Human clone cg4398
c	39	19.4	1.1	34	12	AAQ14188	Probe NT1 based on
c	40	19.4	1.1	40	19	AAV47799	Maize polymorphic
	41	19.4	1.1	41	19	AAV51110	Maize polymorphic
c	42	19.4	1.1	47	16	AAT05673	Primer RD050 for 5
c	43	19.4	1.1	48	11	AAQ05100	Probe including si
	44	19.4	1.1	49	24	ABA98751	Ribosome binding s
	45	19.4	1.1	50	22	AAH25965	Rice genomic fragm

ALIGNMENTS

RESULT 1
AAF75811
ID AAF75811 standard; DNA; 40 BP.
XX
AC AAF75811;
XX
DT 16-MAY-2001 (first entry)
XX
DE Triacylglycerol hydrolase, TGH, oligonucleotide P-TGHI.
XX
KW TGH; triacylglycerol hydrolase; carboxylesterase; EST-1; VLDL; rat;
KW very low density lipoprotein; atherosclerosis; hypercholesterolaemia;
KW hyperbetalipoproteinaemia; non-insulin dependent diabetes mellitus;
KW coronary arterial disease; peripheral vascular disease; pancreatitis;
KW obesity; mixed dyslipidaemia; cerebro-vascular disease; mouse; pig; ss.
XX
OS Mus sp.
OS Rattus sp.
OS Sus scrofa.
XX
PN WO200116358-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-EP08262.
XX
PR 28-AUG-1999; 99GB-0020334.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (UYAL-) UNIV ALBERTA.
XX
PI Borg-Capra CS, Lehner RJ, Vance DE;

XX
DR WPI; 2001-235119/24.
XX
PT Identifying compounds for treating elevated circulating levels of
PT triglyceride, very low density lipoprotein/low density
PT lipoprotein-cholesterol and ApoB-100, comprises identifying
PT triacylglycerol hydrolase inhibitors -
XX
PS Disclosure; Page 10; 28pp; English.
XX
CC The present invention relates to a method for identifying compounds
CC useful in the treatment of conditions resulting from elevated circulating
CC levels of: triglycerides, apoB-100, and/or very low density lipoproteins
CC (VLDL)/ low density lipoproteins (LDL)-cholesterol. The method comprises
CC determining whether the compound inhibits triacylglycerol hydrolase (TGH)
CC activity. TGH has previously been known as carboxylesterase EST-1. It is
CC thought that TGH may participate in the mobilisation of triacylglycerides
CC for assembly into VLDL. Inhibitors of TGH are useful for treating
CC atherosclerosis, hypercholesterolaemia, hyperbetalipoproteinaemia,
CC non-insulin dependent diabetes mellitus (NIDDM), coronary arterial
CC disease, peripheral vascular disease, pancreatitis, obesity, mixed
CC dyslipidaemia and cerebro-vascular disease. The present sequence is an
CC oligonucleotide which was used to clone human TGH (see AAB73263). The
CC present sequence was designed using conserved sites between mouse, rat
CC and pig TGH coding sequences.
XX
SQ Sequence 40 BP; 10 A; 10 C; 13 G; 7 T; 0 other;

Query Match 2.3%; Score 40; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 535 GCATCTGGGGATTCTTCAGCACAGGGGATGAACACAGCCG 574
||||||||||||||||||||||||||||||||||||||||
Db 1 GCATCTGGGGATTCTTCAGCACAGGGGATGAACACAGCCG 40

RESULT 2
AAL33656/c
ID AAL33656 standard; DNA; 50 BP.
XX
AC AAL33656;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #6864.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 3345; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 16 A; 14 C; 10 G; 10 T; 0 other;

Query Match 2.3%; Score 39; DB 22; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.062;
Matches 50; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1076 GGAGTTTGGCTGGTTGATTCCAATGCAGTTGATGAGCTATCCACTCTCCGA 1126
||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 50 GGAGTTTGGCTGGTTGATTCCAATG-AGTTGATGAGCTATCCACTCTCCGA 1

RESULT 3
AAF75812/c
ID AAF75812 standard; DNA; 40 BP.
XX
AC AAF75812;
XX
DT 16-MAY-2001 (first entry)
XX
DE Triacylglycerol hydrolase, TGH, oligonucleotide P-TGHII.
XX
KW TGH; triacylglycerol hydrolase; carboxylesterase; EST-1; VLDL; rat;
KW very low density lipoprotein; atherosclerosis; hypercholesterolaemia;
KW hyperbetalipoproteinaemia; non-insulin dependent diabetes mellitus;
KW coronary arterial disease; peripheral vascular disease; pancreatitis;
KW obesity; mixed dyslipidaemia; cerebro-vascular disease; mouse; pig; ss.
XX
OS Mus sp.
OS Rattus sp.
OS Sus scrofa.
XX
PN WO200116358-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-EP08262.
XX
PR 28-AUG-1999; 99GB-0020334.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (UYAL-) UNIV ALBERTA.
XX
PI Borg-Capra CS, Lehner RJ, Vance DE;
XX
DR WPI; 2001-235119/24.
XX
PT Identifying compounds for treating elevated circulating levels of
PT triglyceride, very low density lipoprotein/low density
PT lipoprotein-cholesterol and ApoB-100, comprises identifying
PT triacylglycerol hydrolase inhibitors -

```
XX
PS   Disclosure; Page 10; 28pp; English.
XX
CC   The present invention relates to a method for identifying compounds
CC   useful in the treatment of conditions resulting from elevated circulating
CC   levels of: triglycerides, apoB-100, and/or very low density lipoproteins
CC   (VLDL)/ low density lipoproteins (LDL)-cholesterol. The method comprises
CC   determining whether the compound inhibits triacylglycerol hydrolase (TGH)
CC   activity. TGH has previously been known as carboxylesterase EST-1. It is
CC   thought that TGH may participate in the mobilisation of triacylglycerides
CC   for assembly into VLDL. Inhibitors of TGH are useful for treating
CC   atherosclerosis, hypercholesterolaemia, hyperbetalipoproteinaemia,
CC   non-insulin dependent diabetes mellitus (NIDDM), coronary arterial
CC   disease, peripheral vascular disease, pancreatitis, obesity, mixed
CC   dyslipidaemia and cerebro-vascular disease. The present sequence is an
CC   oligonucleotide which was used to clone human TGH (see AAB73263). The
CC   present sequence was designed using conserved sites between mouse, rat
CC   and pig TGH coding sequences.
XX
SQ   Sequence 40 BP; 10 A; 9 C; 9 G; 12 T; 0 other;

  Query Match             2.0%;  Score 35.2;  DB 22;  Length 40;
  Best Local Similarity   92.5%;  Pred. No. 0.83;
  Matches   37;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy   1491 CTTAGCAAGATGGTGATGAAATTCTGGGCCAACTTTGCTC 1530
           || ||||| |||||||||||||| ||||||||||||||||
Db     40 CTCAGCAAAATGGTGATGAAATACTGGGCCAACTTTGCTC 1

RESULT 4
ABT04547
ID   ABT04547 standard; DNA; 30 BP.
XX
AC   ABT04547;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Human CES1 gene probe SEQ ID NO: 13.
XX
KW   Human; drug metabolism; enzyme; probe; ss.
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OS   Homo sapiens.
XX
PN   JP2002142780-A.
XX
PD   21-MAY-2002.
XX
PF   28-AUG-2001; 2001JP-0257338.
XX
PR   04-SEP-2000; 2000JP-0267163.
XX
PA   (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX
DR   WPI; 2002-552472/59.
XX
PT   Measurement of an enzyme participating to the first phase reaction of
PT   drug metabolism, a probe and a kit for it  -
XX
PS   Claim 4; Page 18; 36pp; Japanese.
XX
CC   The present invention relates to probes which can be used for the
CC   measurement of an enzyme. The probes can be used for the measurement of
CC   an enzyme participating to the first phase reaction of drug metabolism.
CC   The present sequence is a probe shown in the invention.
XX
SQ   Sequence 30 BP; 9 A; 7 C; 7 G; 7 T; 0 other;

  Query Match             1.7%;  Score 30;  DB 24;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    993 ATGCTGCTGCTGAAAACACCTGAAGAGCTT 1022
          ||||||||||||||||||||||||||||||
Db      1 ATGCTGCTGCTGAAAACACCTGAAGAGCTT 30

RESULT 5
AAF75814/c
ID   AAF75814 standard; DNA; 25 BP.
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AC   AAF75814;
XX
DT   16-MAY-2001  (first entry)
XX
DE   Triacylglycerol hydrolase, TGH, oligonucleotide hCE3'Rev.
XX
KW   TGH; triacylglycerol hydrolase; carboxylesterase; EST-1; VLDL;
KW   very low density lipoprotein; atherosclerosis; hypercholesterolaemia;
KW   hyperbetalipoproteinaemia; non-insulin dependent diabetes mellitus;
KW   coronary arterial disease; peripheral vascular disease; pancreatitis;
KW   obesity; mixed dyslipidaemia; cerebro-vascular disease; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116358-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-EP08262.
XX
PR   28-AUG-1999;   99GB-0020334.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (UYAL-) UNIV ALBERTA.
XX
PI   Borg-Capra CS,  Lehner RJ,  Vance DE;
XX
DR   WPI; 2001-235119/24.
XX
PT   Identifying compounds for treating elevated circulating levels of
PT   triglyceride, very low density lipoprotein/low density
PT   lipoprotein-cholesterol and ApoB-100, comprises identifying
PT   triacylglycerol hydrolase inhibitors  -
XX
PS   Disclosure; Page 11; 28pp; English.
XX
CC   The present invention relates to a method for identifying compounds
CC   useful in the treatment of conditions resulting from elevated circulating
CC   levels of: triglycerides, apoB-100, and/or very low density lipoproteins
CC   (VLDL)/ low density lipoproteins (LDL)-cholesterol. The method comprises
CC   determining whether the compound inhibits triacylglycerol hydrolase (TGH)
CC   activity. TGH has previously been known as carboxylesterase EST-1. It is
CC   thought that TGH may participate in the mobilisation of triacylglycerides
CC   for assembly into VLDL. Inhibitors of TGH are useful for treating
CC   atherosclerosis, hypercholesterolaemia, hyperbetalipoproteinaemia,
CC   non-insulin dependent diabetes mellitus (NIDDM), coronary arterial
CC   disease, peripheral vascular disease, pancreatitis, obesity, mixed
CC   dyslipidaemia and cerebro-vascular disease. The present sequence is an
CC   oligonucleotide which was used to clone human TGH (see AAB73263). The
CC   present sequence corresponds to the 3' end of human carboxylesterase I
CC   (hCEI).
XX
SQ   Sequence 25 BP; 3 A; 6 C; 6 G; 10 T; 0 other;

  Query Match             1.4%;  Score 25;  DB 22;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1697 CCAGACAGAACACATAGAGCTGTGA 1721
           |||||||||||||||||||||||||
Db     25 CCAGACAGAACACATAGAGCTGTGA 1

RESULT 6
AAZ34198/c
```

```
ID   AAZ34198 standard; DNA; 50 BP.
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AC   AAZ34198;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human PRO237 hybridisation probe.
XX
KW   Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW   probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW   secreted protein; transmembrane protein; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9946281-A2.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05028.
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PR   10-MAR-1998;   98US-0077450.
PR   11-MAR-1998;   98US-0077632.
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PR   13-MAR-1998;   98US-0078004.
PR   17-MAR-1998;   98US-0040220.
PR   20-MAR-1998;   98US-0078886.
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PR   25-MAR-1998;   98US-0079294.
PR   26-MAR-1998;   98US-0079656.
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PR   27-MAR-1998;   98US-0079664.
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PR   30-MAR-1998;   98US-0079920.
PR   30-MAR-1998;   98US-0079923.
PR   31-MAR-1998;   98US-0080105.
PR   31-MAR-1998;   98US-0080107.
PR   31-MAR-1998;   98US-0080165.
PR   31-MAR-1998;   98US-0080194.
PR   01-APR-1998;   98US-0080327.
PR   01-APR-1998;   98US-0080328.
PR   01-APR-1998;   98US-0080333.
PR   01-APR-1998;   98US-0080334.
PR   08-APR-1998;   98US-0081049.
PR   08-APR-1998;   98US-0081070.
PR   08-APR-1998;   98US-0081071.
PR   09-APR-1998;   98US-0081195.
PR   09-APR-1998;   98US-0081203.
PR   09-APR-1998;   98US-0081229.
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PR   15-APR-1998;   98US-0081838.
PR   15-APR-1998;   98US-0081952.
PR   15-APR-1998;   98US-0081955.
PR   21-APR-1998;   98US-0082568.
PR   21-APR-1998;   98US-0082569.
PR   22-APR-1998;   98US-0082700.
PR   22-APR-1998;   98US-0082704.
PR   22-APR-1998;   98US-0082804.
PR   23-APR-1998;   98US-0082767.
PR   23-APR-1998;   98US-0082796.
PR   27-APR-1998;   98US-0083336.
PR   28-APR-1998;   98US-0083322.
PR   29-APR-1998;   98US-0083392.
PR   29-APR-1998;   98US-0083495.
PR   29-APR-1998;   98US-0083496.
PR   29-APR-1998;   98US-0083499.
PR   29-APR-1998;   98US-0083500.
PR   29-APR-1998;   98US-0083545.
PR   29-APR-1998;   98US-0083554.
PR   29-APR-1998;   98US-0083558.
PR   29-APR-1998;   98US-0083559.
PR   30-APR-1998;   98US-0083742.
PR   05-MAY-1998;   98US-0084366.
PR   06-MAY-1998;   98US-0084414.
PR   06-MAY-1998;   98US-0084441.
PR   07-MAY-1998;   98US-0084598.
PR   07-MAY-1998;   98US-0084600.
PR   07-MAY-1998;   98US-0084627.
PR   07-MAY-1998;   98US-0084637.
PR   07-MAY-1998;   98US-0084639.
PR   07-MAY-1998;   98US-0084640.
PR   07-MAY-1998;   98US-0084643.
PR   13-MAY-1998;   98US-0085323.
PR   13-MAY-1998;   98US-0085338.
PR   13-MAY-1998;   98US-0085339.
PR   15-MAY-1998;   98US-0085573.
PR   15-MAY-1998;   98US-0085579.
PR   15-MAY-1998;   98US-0085580.
PR   15-MAY-1998;   98US-0085582.
PR   15-MAY-1998;   98US-0085689.
PR   15-MAY-1998;   98US-0085697.
PR   15-MAY-1998;   98US-0085700.
PR   15-MAY-1998;   98US-0085704.
PR   18-MAY-1998;   98US-0086023.
PR   22-MAY-1998;   98US-0086392.
PR   22-MAY-1998;   98US-0086414.
PR   22-MAY-1998;   98US-0086430.
PR   22-MAY-1998;   98US-0086486.
PR   28-MAY-1998;   98US-0087098.
PR   28-MAY-1998;   98US-0087106.
PR   28-MAY-1998;   98US-0087208.
PR   30-JUL-1998;   98US-0094651.
PR   11-SEP-1998;   98US-0100038.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wood WI,  Goddard A,  Gurney A,  Yuan J,  Baker KP,  Chen J;
XX
DR   WPI; 1999-551358/46.
XX
PT   New secreted and transmembrane polypeptides and their polynucleotides,
PT   useful for treating blood coagulation disorders, cancers and cellular
PT   adhesion disorders -
XX
PS   Example 55; Page 228; 530pp; English.
XX
CC   The present invention describes secreted and transmembrane polypeptides
CC   and their polynucleotides. The nucleotide sequences are useful as
CC   sources of probes, primers, for chromosome mapping, and for generation
CC   of antisense sequences. They can also be used to create transgenic
CC   animals. The proteins can be used to treat a variety of diseases and
CC   disorders, depending on their function. Diseases that may be treated
CC   include blood coagulation disorders, cancers and cellular adhesion
CC   disorders. They may also be used to raise antibodies. AAZ33891 to
CC   AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC   polypeptide sequence given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;

  Query Match             1.3%;  Score 22.4;  DB 20;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 9.1e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
           || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


RESULT 7
```

AAC78815/c
ID AAC78815 standard; DNA; 50 BP.
XX
AC AAC78815;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO237 hybridisation probe SEQ ID NO:361.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Example 55; Page 285; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;

Query Match 1.3%; Score 22.4; DB 21; Length 50;
Best Local Similarity 66.7%; Pred. No. 9.1e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
|| || |||||| ||| | |||| || | | || || |||| ||
Db 50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3

RESULT 8
AAC58128/c
ID AAC58128 standard; DNA; 50 BP.
XX
AC AAC58128;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO237 hybridisation probe SEQ ID NO:39.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
KW tumourigenesis; detection; neoplastic cell growth; proliferation;
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
KW immunological disorder; hybridisation; probe; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200053754-A1.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US00277.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 05-OCT-1999; 99WO-US23089.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
PI Wood WI;
XX
DR WPI; 2000-572269/53.
XX
PT New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment -
XX
PS Example 2; Page 95; 195pp; English.
XX
CC The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO538, PRO3664, PRO618,
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
CC and methods for the diagnosis and treatment of neoplastic cell growth
CC and proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumour cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumour treatment. Compounds
CC that inhibit the expression or activity of the identified polypeptides
CC can be identified and used as antagonists. Benign or malignant tumours,
CC inflammatory disorders and immunological disorders can be treated.
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;

Query Match 1.3%; Score 22.4; DB 21; Length 50;

```
  Best Local Similarity   66.7%;  Pred. No. 9.1e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
           || || |||||| |||   |  |||| || | | ||  || |||| ||
Db      50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


RESULT 9
AAA88445/c
ID   AAA88445 standard; DNA; 50 BP.
XX
AC   AAA88445;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antitumour PRO237 gene hydridisation probe 30905.p.
XX
KW   PRO237; antitumour; antiproliferative; human; cancer; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200053751-A1.
XX
PD   14-SEP-2000.
XX
PF   30-DEC-1999;   99WO-US31243.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   29-MAR-1999;   99US-0126773.
PR   20-JUL-1999;   99US-0144758.
PR   08-SEP-1999;   99WO-US20594.
PR   20-DEC-1999;   99WO-US30999.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Napier MA,  Wood WI;
XX
DR   WPI; 2000-594321/56.
XX
PT   Novel PRO181 and PRO237 polypeptides useful for treating tumors
PT   including cancers of breast, prostate, lung, leukemia in humans and for
PT   identifying compounds capable of inhibiting growth of neoplastic cells
PT   -
XX
PS   Example 1; Page 76; 107pp; English.
XX
CC   This hybridisation probe, termed 30905.p, is based on consensus
CC   sequence DNA30905.  This consensus sequence was produced from
CC   clones isolated following an expressed sequence tag screening using
CC   the extracellular domain of 950 known secreted proteins.  The
CC   probe was used to screen several cDNA libraries.  A cDNA clone (see
CC   AAA88440) encoding human PRO237 (see AAB19525), a novel inhibitor of
CC   neoplastic cell growth, was obtained from a human foetal brain
CC   tissue cDNA library.
XX
SQ   Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;

  Query Match             1.3%;  Score 22.4;  DB 21;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 9.1e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
           || || |||||| |||   |  |||| || | | ||  || |||| ||
Db      50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


RESULT 10
AAZ66351/c
ID   AAZ66351 standard; DNA; 47 BP.
XX
AC   AAZ66351;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:698.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 379; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 13 A; 9 C; 11 G; 14 T; 0 other;

  Query Match             1.3%;  Score 22.2;  DB 21;  Length 47;
  Best Local Similarity   77.1%;  Pred. No. 1e+04;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    1148 AGCCATGTCACTCCTGTGGAAGTCCTATCCCCTTG 1182
           ||| | ||| || ||||| |||||  | |||||||
Db      41 AGCTAAGTCTCTTCTGTGAAAGTCAAAGCCCCTTG 7


RESULT 11
ABT04612
ID   ABT04612 standard; DNA; 22 BP.
XX
AC   ABT04612;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Human CES1 gene probe SEQ ID NO: 78.
```

```
XX
KW   Human; drug metabolism; enzyme; probe; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002142780-A.
XX
PD   21-MAY-2002.
XX
PF   28-AUG-2001; 2001JP-0257338.
XX
PR   04-SEP-2000; 2000JP-0267163.
XX
PA   (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX
DR   WPI; 2002-552472/59.
XX
PT   Measurement of an enzyme participating to the first phase reaction of
PT   drug metabolism, a probe and a kit for it  -
XX
PS   Claim 8; Page 26; 36pp; Japanese.
XX
CC   The present invention relates to probes which can be used for the
CC   measurement of an enzyme. The probes can be used for the measurement of
CC   an enzyme participating to the first phase reaction of drug metabolism.
CC   The present sequence is a probe shown in the invention.
XX
SQ   Sequence 22 BP; 6 A; 8 C; 4 G; 4 T; 0 other;

  Query Match             1.3%;  Score 22;  DB 24;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+03;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     952 CCAGAGAGAGTCAACCCCTTCT 973
           ||||||||||||||||||||||
Db       1 CCAGAGAGAGTCAACCCCTTCT 22


RESULT 12
AAT68598
ID   AAT68598 standard; DNA; 35 BP.
XX
AC   AAT68598;
XX
DT   08-AUG-1997  (first entry)
XX
DE   Md-alpha-E7 gene primer Md1.
XX
KW   Malathion carboxylesterase; organophosphate; insecticide;
KW   pesticide; remediation; bioremediation; decontamination;
KW   Musca domestica; polymerase chain reaction; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    9
FT                    /*tag=  a
FT                    /mod_base= i
FT   modified_base    12
FT                    /*tag=  b
FT                    /mod_base= i
FT   modified_base    15
FT                    /*tag=  c
FT                    /mod_base= i
FT   modified_base    21
FT                    /*tag=  d
FT                    /mod_base= i
FT   modified_base    27
FT                    /*tag=  e
FT                    /mod_base= i
FT   modified_base    30
FT                    /*tag=  f
FT                    /mod_base= i
XX
PN   WO9719176-A1.
XX
PD   29-MAY-1997.
XX
PF   22-NOV-1996;   96WO-AU00746.
XX
PR   23-NOV-1995;   95AU-0006751.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Boyce T,  Brownlie JC,  Campbell PM,  Claudianos C;
PI   Newcomb RD,  Oakeshott JG,  Robin GC,  Russell RJ,  Smyth K;
XX
DR   WPI; 1997-298113/27.
XX
PT   DNA encoding enzyme that degrades organophosphate pesticides -
PT   useful for decontamination of soil, water, food etc
XX
PS   Disclosure; Page 14; 52pp; English.
XX
CC   Consensus generic alpha-esterase primers (AAT68598-99) were designed
CC   to the conserved regions of multiple amino acid alignments of
CC   Drosophila melanogaster and Lucilia cuprina alpha-esterase
CC   genes (see also AAT68596), and used in a PCR amplification of
CC   Musca domestica genomic DNA.  Primer Md1 corresponds to residues
CC   58-69 of L. cuprina alpha-E7 and Md2 to nucleotides 92-83.  A 540
CC   bp amplicon was used to screen a M. domestica genomic library to
CC   isolate the Md alpha-E7 gene (AAT68597).
XX
SQ   Sequence 35 BP; 4 A; 8 C; 7 G; 5 T; 11 other;

  Query Match             1.2%;  Score 21.2;  DB 18;  Length 35;
  Best Local Similarity   60.0%;  Pred. No. 1.7e+04;
  Matches   21;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     165 TTCCTGGGAATCCCTTTTGCCAAGCCGCCTCTTGG 199
           |||  ||| || || | :|| :|:|| || :| ||
Db       1 TTCGAGGGNATNCCNTAYGCNMARCCNCCNBTNGG 35


RESULT 13
ABL52742/c
ID   ABL52742 standard; DNA; 41 BP.
XX
AC   ABL52742;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Nucleophosmin 9.68 associated probe 1.
XX
KW   Nucleophosmin 9.68; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; malignant tumour; haemopathy; HIV;
KW   immunological disease; inflammatory disease; probe; ss.
XX
OS   Unidentified.
XX
PN   WO200206471-A1.
XX
PD   24-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-CN01074.
XX
PR   30-JUN-2000; 2000CN-0116971.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-122632/16.
XX
PT   Nucleophosmin 9.68 polynucleotide and polypeptide, useful in diagnosis
PT   and treatment of malignant tumour, haemopathy, HIV infection,
```

```
PT   immunological diseases and various inflammatory diseases -
XX
PS   Example 6; Page 21; 36pp; Chinese.
XX
CC   The invention relates to an isolated nucleophosmin 9.68 polypeptide.
CC   The activity of the protein of the invention may be described as,
CC   cytostatic, virucidal, immunomodulatory, antiinflammatory and
CC   haemostatic. The polypeptide and encoded polynucleotide are applicable in
CC   diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC   immunological diseases and various inflammatory diseases. The screened
CC   compounds as well as their preparations are also useful for treating
CC   the diseases mentioned above. The current sequence represents a
CC   nucleophosmin 9.68 associated probe.
XX
SQ   Sequence 41 BP; 8 A; 10 C; 13 G; 10 T; 0 other;

  Query Match             1.2%;  Score 21.2;  DB 24;  Length 41;
  Best Local Similarity   88.5%;  Pred. No. 1.9e+04;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     565 AACACAGCCGGGGGAACTGGGGTCAC 590
           ||||||||||  ||||||||| ||||
Db      41 AACACAGCCGTTGGAACTGGGCTCAC 16


RESULT 14
ABL52743/c
ID   ABL52743 standard; DNA; 41 BP.
XX
AC   ABL52743;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Nucleophosmin 9.68 associated probe 2.
XX
KW   Nucleophosmin 9.68; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; malignant tumour; haemopathy; HIV;
KW   immunological disease; inflammatory disease; probe; ss.
XX
OS   Unidentified.
XX
PN   WO200206471-A1.
XX
PD   24-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-CN01074.
XX
PR   30-JUN-2000; 2000CN-0116971.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-122632/16.
XX
PT   Nucleophosmin 9.68 polynucleotide and polypeptide, useful in diagnosis
PT   and treatment of malignant tumour, haemopathy, HIV infection,
PT   immunological diseases and various inflammatory diseases -
XX
PS   Example 6; Page 21; 36pp; Chinese.
XX
CC   The invention relates to an isolated nucleophosmin 9.68 polypeptide.
CC   The activity of the protein of the invention may be described as,
CC   cytostatic, virucidal, immunomodulatory, antiinflammatory and
CC   haemostatic. The polypeptide and encoded polynucleotide are applicable in
CC   diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC   immunological diseases and various inflammatory diseases. The screened
CC   compounds as well as their preparations are also useful for treating
CC   the diseases mentioned above. The current sequence represents a
CC   nucleophosmin 9.68 associated probe.
XX
SQ   Sequence 41 BP; 8 A; 10 C; 13 G; 10 T; 0 other;

  Query Match             1.2%;  Score 21.2;  DB 24;  Length 41;
  Best Local Similarity   88.5%;  Pred. No. 1.9e+04;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     565 AACACAGCCGGGGGAACTGGGGTCAC 590
           ||||||||||  ||||||||| ||||
Db      41 AACACAGCCGTTGGAACTGGGCTCAC 16


RESULT 15
ABT04613/c
ID   ABT04613 standard; DNA; 21 BP.
XX
AC   ABT04613;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Human CES1 gene probe SEQ ID NO: 79.
XX
KW   Human; drug metabolism; enzyme; probe; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002142780-A.
XX
PD   21-MAY-2002.
XX
PF   28-AUG-2001; 2001JP-0257338.
XX
PR   04-SEP-2000; 2000JP-0267163.
XX
PA   (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX
DR   WPI; 2002-552472/59.
XX
PT   Measurement of an enzyme participating to the first phase reaction of
PT   drug metabolism, a probe and a kit for it  -
XX
PS   Claim 8; Page 26; 36pp; Japanese.
XX
CC   The present invention relates to probes which can be used for the
CC   measurement of an enzyme. The probes can be used for the measurement of
CC   an enzyme participating to the first phase reaction of drug metabolism.
CC   The present sequence is a probe shown in the invention.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 3 G; 8 T; 0 other;

  Query Match             1.2%;  Score 21;  DB 24;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1058 GGTCGGAATTAACAAGCAGGA 1078
           |||||||||||||||||||||
Db      21 GGTCGGAATTAACAAGCAGGA 1

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Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21.2	1.2	35	4	US-09-068-960-30	Sequence 30, Appl
c	2	20.6	1.2	35	1	US-08-805-814-3	Sequence 3, Appli
c	3	20.6	1.2	35	1	US-08-484-815-3	Sequence 3, Appli
c	4	20.6	1.2	35	3	US-08-888-949-3	Sequence 3, Appli
c	5	20.6	1.2	35	4	US-08-888-950-3	Sequence 3, Appli
c	6	20.6	1.2	35	4	US-09-262-758-3	Sequence 3, Appli
c	7	20.6	1.2	35	5	PCT-US95-10284-3	Sequence 3, Appli
c	8	20.2	1.2	30	1	US-08-073-799C-6	Sequence 6, Appli
c	9	20.2	1.2	30	1	US-07-946-232-6	Sequence 6, Appli
c	10	20.2	1.2	30	1	US-07-947-672-6	Sequence 6, Appli
c	11	20.2	1.2	30	1	US-08-432-043-6	Sequence 6, Appli
c	12	20.2	1.2	30	2	US-08-660-963-6	Sequence 6, Appli
c	13	20	1.2	47	3	US-09-264-737-8	Sequence 8, Appli
c	14	19.4	1.1	39	3	US-08-907-598-4	Sequence 4, Appli
c	15	19.4	1.1	47	1	US-08-426-020-3	Sequence 3, Appli
c	16	19.2	1.1	43	1	US-07-988-194A-25	Sequence 25, Appl
c	17	19.2	1.1	43	1	US-08-258-152-27	Sequence 27, Appl
c	18	19.2	1.1	43	2	US-08-076-299A-27	Sequence 27, Appl
c	19	19.2	1.1	43	2	US-08-438-582-27	Sequence 27, Appl
c	20	19.2	1.1	43	4	US-09-266-596-27	Sequence 27, Appl
c	21	19.2	1.1	43	4	US-08-479-737-25	Sequence 25, Appl
c	22	19.2	1.1	43	4	US-08-475-442A-25	Sequence 25, Appl
	23	19.2	1.1	49	1	US-08-258-188-3	Sequence 3, Appli
c	24	19.2	1.1	49	1	US-08-258-188-28	Sequence 28, Appl
	25	19.2	1.1	49	1	US-08-258-188-29	Sequence 29, Appl
	26	19.2	1.1	49	1	US-08-526-813-3	Sequence 3, Appli
c	27	19.2	1.1	49	1	US-08-526-813-28	Sequence 28, Appl
	28	19.2	1.1	49	1	US-08-526-813-29	Sequence 29, Appl
	29	19.2	1.1	49	5	PCT-US95-08554-3	Sequence 3, Appli
c	30	19.2	1.1	49	5	PCT-US95-08554-28	Sequence 28, Appl
	31	19.2	1.1	49	5	PCT-US95-08554-29	Sequence 29, Appl
c	32	19	1.1	36	1	US-08-805-814-4	Sequence 4, Appli
c	33	19	1.1	36	1	US-08-484-815-4	Sequence 4, Appli
c	34	19	1.1	36	3	US-08-888-949-4	Sequence 4, Appli
c	35	19	1.1	36	4	US-08-888-950-4	Sequence 4, Appli
c	36	19	1.1	36	4	US-09-262-758-4	Sequence 4, Appli
c	37	19	1.1	36	5	PCT-US95-10284-4	Sequence 4, Appli
c	38	19	1.1	47	3	US-08-726-807B-21	Sequence 21, Appl
c	39	19	1.1	47	3	US-09-258-367-21	Sequence 21, Appl
c	40	19	1.1	47	4	US-09-546-550-21	Sequence 21, Appl
c	41	19	1.1	47	4	US-09-431-414-21	Sequence 21, Appl
c	42	19	1.1	47	4	US-09-225-670-21	Sequence 21, Appl
c	43	19	1.1	47	4	US-09-431-349C-21	Sequence 21, Appl
	44	19	1.1	49	1	US-08-484-493-4	Sequence 4, Appli
	45	19	1.1	49	1	US-08-484-494-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-068-960-30
; Sequence 30, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
;  APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
;  TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
;  FILE REFERENCE: Attorney Docket No. 6235515 50179-051
;  CURRENT APPLICATION NUMBER: US/09/068,960A
;  CURRENT FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: PCT/AU96/00746
;  EARLIER FILING DATE: 1996-11-22
;  EARLIER APPLICATION NUMBER: AU 6751
;  EARLIER FILING DATE: 1995-11-23
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 35
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Degenerate
;   OTHER INFORMATION: Primer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (9)
;   OTHER INFORMATION: i
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (12)
;   OTHER INFORMATION: i
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (15)
;   OTHER INFORMATION: i
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (21)
;   OTHER INFORMATION: i
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (27)
;   OTHER INFORMATION: i
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (30)
;   OTHER INFORMATION: i
US-09-068-960-30

  Query Match                 1.2%;  Score 21.2;  DB 4;  Length 35;
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Db       1 TTCGAGGGNATNCCNTAYGCNMARCCNCCNBTNGG 35


RESULT 2
US-08-805-814-3/c
; Sequence 3, Application US/08805814
; Patent No. 5716820
;  GENERAL INFORMATION:
;    APPLICANT:  Duvick, Jon
;    APPLICANT:  Rood, Tracy A.
;    APPLICANT:  Wang, Xun
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  IA
;      COUNTRY:  USA
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Windows 3.1 - No. 5716820epad
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,814
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roth, Michael J.
;      REGISTRATION NUMBER:  29,342
;      REFERENCE/DOCKET NUMBER:  0272 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515-248-4895
;      TELEFAX:  515-248-4934
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 bases
;      TYPE:  nucleotide
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  probe
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-805-814-3

  Query Match             1.2%;  Score 20.6;  DB 1;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 3
US-08-484-815-3/c
; Sequence 3, Application US/08484815
; Patent No. 5792931
;  GENERAL INFORMATION:
;    APPLICANT:  DUVICK, JONATHAN
;    APPLICANT:  ROOD, TRACY A.
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION COMPOSITIONS
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  USA
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,815
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bobrowicz, Donna I.
;      REGISTRATION NUMBER:  32,196
;      REFERENCE/DOCKET NUMBER:  0272 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515 248-4895
;      TELEFAX:  515 248-4934
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-484-815-3

  Query Match             1.2%;  Score 20.6;  DB 1;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 4
US-08-888-949-3/c
; Sequence 3, Application US/08888949
; Patent No. 6025188
;  GENERAL INFORMATION:
;    APPLICANT:  Duvick, Jonathan
;    APPLICANT:  Maddox, Joyce R.
;    APPLICANT:  Rood, Tracy A.
;    APPLICANT:  Wang, Xun
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION COMPOSITIONS
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PIONEER HI-BRED INTERNATIONAL, INC.
;      STREET:  Darwin Building, 7100 N.W. 62nd Ave., P.O.
;      STREET:  Box 1000
;      CITY:  Johnston
;      STATE:  Iowa
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,949
;      FILING DATE:  07-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/484,815
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/289,595
```

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;      FILING DATE:  12-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweeney, Patricia A.
;      REGISTRATION NUMBER:  32,733
;      REFERENCE/DOCKET NUMBER:  272R3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (515) 248-4800
;      TELEFAX:  (515) 248-4844
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-949-3

  Query Match             1.2%;  Score 20.6;  DB 3;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
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Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 5
US-08-888-950-3/c
; Sequence 3, Application US/08888950
; Patent No. 6229071
;  GENERAL INFORMATION:
;    APPLICANT:  Duvick, Jonathan
;    APPLICANT:  Maddox, Joyce R.
;    APPLICANT:  Rood, Tracy A.
;    APPLICANT:  Wang, Xun
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION COMPOSITIONS
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PIONEER HI-BRED INTERNATIONAL, INC.
;      STREET:  Darwin Building, 7100 N.W. 62nd Ave., P.O.
;      STREET:  Box 1000
;      CITY:  Johnston
;      STATE:  Iowa
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,950
;      FILING DATE:  07-JUL-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/484,815
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/289,595
;      FILING DATE:  12-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweeney, Patricia A.
;      REGISTRATION NUMBER:  32,733
;      REFERENCE/DOCKET NUMBER:  272R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (515) 248-4800
;      TELEFAX:  (515) 248-4844
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-950-3

  Query Match             1.2%;  Score 20.6;  DB 4;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
           ||:||:|| :  ||:|| || :|:||| |||
Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 6
US-09-262-758-3/c
; Sequence 3, Application US/09262758
; Patent No. 6239330
;  GENERAL INFORMATION:
;    APPLICANT:  Duvick, Jonathan
;    APPLICANT:  Maddox, Joyce R.
;    APPLICANT:  Rood, Tracy A.
;    APPLICANT:  Wang, Xun
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION COMPOSITIONS
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PIONEER HI-BRED INTERNATIONAL, INC.
;      STREET:  Darwin Building, 7100 N.W. 62nd Ave., P.O.
;      STREET:  Box 1000
;      CITY:  Johnston
;      STATE:  Iowa
;      COUNTRY:  USA
;      ZIP:  50131
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/262,758
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/484,815
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/289,595
;      FILING DATE:  12-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweeney, Patricia A.
;      REGISTRATION NUMBER:  32,733
;      REFERENCE/DOCKET NUMBER:  272R3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (515) 248-4800
;      TELEFAX:  (515) 248-4844
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-262-758-3

  Query Match             1.2%;  Score 20.6;  DB 4;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
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Db      35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5
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RESULT 7
PCT-US95-10284-3/c
; Sequence 3, Application PC/TUS9510284
;  GENERAL INFORMATION:
;    APPLICANT:  PIONEER HI-BRED INTERNATIONAL, INC.
;    TITLE OF INVENTION:  FUMONISIN DETOXIFICATION COMPOSITIONS
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pioneer Hi-Bred International
;      STREET:  700 Capital Square, 400 Locust Street
;      CITY:  Des Moines
;      STATE:  Iowa
;      COUNTRY:  USA
;      ZIP:  50309
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/10284
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bobrowicz, Donna I.
;      REGISTRATION NUMBER:  32,196
;      REFERENCE/DOCKET NUMBER:  0272-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  515 248-4895
;      TELEFAX:  515 248-4844
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-10284-3

  Query Match             1.2%;  Score 20.6;  DB 5;  Length 35;
  Best Local Similarity   61.3%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
          ||:||:|| :  ||:|| || :|:||| |||
Db     35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5


RESULT 8
US-08-073-799C-6/c
; Sequence 6, Application US/08073799C
; Patent No. 5583010
;  GENERAL INFORMATION:
;    APPLICANT:  Zysk, John R.
;    APPLICANT:  Baumbach, William R.
;    APPLICANT:  Thorner, Michael O.
;    APPLICANT:  Gaylinn, Bruce D.
;    APPLICANT:  Lynch, Kevin R.
;    APPLICANT:  Harrison, Jeffrey K.
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND
;    TITLE OF INVENTION:  PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING HORMONE REC
;    TITLE OF INVENTION:  AND CLONING OF A GENE ENCODING FOR THE GROWTH HORMONE RELEASIN
;    TITLE OF INVENTION:  HORMONE RECEPTOR
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
;      STREET:  Metropolitan Square Building, Suite 800, 1450 G St., N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/073,799C
;      FILING DATE:  June 10, 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/902,826
;      FILING DATE:  23-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  O'Shaughnessy, Brian P.
;      REGISTRATION NUMBER:  32,747
;      REFERENCE/DOCKET NUMBER:  1574/81-2216
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-824-8000
;      TELEFAX:  202-824-8199
;      TELEX:  248516
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-073-799C-6

  Query Match             1.2%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 4.5e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
          || |||||||||| ||||| |||||
Db     30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


RESULT 9
US-07-946-232-6/c
; Sequence 6, Application US/07946232
; Patent No. 5591641
;  GENERAL INFORMATION:
;    APPLICANT:  Thorner, Michael O.
;    APPLICANT:  Gaylinn, Bruce D.
;    APPLICANT:  Lynch, Kevin R.
;    APPLICANT:  Harrison, Jeffrey K.
;    APPLICANT:  Zysk, John R.
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND
;    TITLE OF INVENTION:  PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING
;    TITLE OF INVENTION:  HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE
;    TITLE OF INVENTION:  GROWTH HORMONE RELEASING HORMONE RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MASON, FENWICK & LAWRENCE
;      STREET:  1225 I Street, N.W., Suite 1000
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,232
;      FILING DATE:  19920915
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/902,826
;      FILING DATE:  23-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schein, Daniel B.
;      REGISTRATION NUMBER:  33,551
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;      REFERENCE/DOCKET NUMBER:  1084/81-1317
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-289-1200
;      TELEFAX:  202-289-6674
;      TELEX:  248516
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-946-232-6

  Query Match             1.2%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 4.5e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
           || |||||||||| ||||| |||||
Db      30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


RESULT 10
US-07-947-672-6/c
; Sequence 6, Application US/07947672
; Patent No. 5612470
;  GENERAL INFORMATION:
;    APPLICANT:  Thorner, Michael O.
;    APPLICANT:  Gaylinn, Bruce D.
;    APPLICANT:  Lynch, Kevin R.
;    APPLICANT:  Harrison, Jeffrey K.
;    APPLICANT:  Zysk, John R.
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND
;    TITLE OF INVENTION:  PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING
;    TITLE OF INVENTION:  HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE
;    TITLE OF INVENTION:  GROWTH HORMONE RELEASING HORMONE RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MASON, FENWICK & LAWRENCE
;      STREET:  1225 I Street, N.W., Suite 1000
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,672
;      FILING DATE:  19920918
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/902,826
;      FILING DATE:  23-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schein, Daniel B.
;      REGISTRATION NUMBER:  33,551
;      REFERENCE/DOCKET NUMBER:  1084/81-1365
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-289-1200
;      TELEFAX:  202-289-6674
;      TELEX:  248516
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-947-672-6

  Query Match             1.2%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 4.5e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
           || |||||||||| ||||| |||||
Db      30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


RESULT 11
US-08-432-043-6/c
; Sequence 6, Application US/08432043
; Patent No. 5644046
;  GENERAL INFORMATION:
;    APPLICANT:  Thorner, Michael O.
;    APPLICANT:  Gaylinn, Bruce D.
;    APPLICANT:  Lynch, Kevin R.
;    APPLICANT:  Harrison, Jeffrey K.
;    APPLICANT:  Zysk, John R.
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND
;    TITLE OF INVENTION:  PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING
;    TITLE OF INVENTION:  HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE
;    TITLE OF INVENTION:  GROWTH HORMONE RELEASING HORMONE RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  POPHAM HAIK SCHNOBRICH & KAUFMAN, LTD.
;      STREET:  655 15th Street, N.W., Suite 800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/432,043
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/947,672
;      FILING DATE:  18-SEP-1992
;      APPLICATION NUMBER:  US 07/902,826
;      FILING DATE:  23-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  O'Shaughnessy, Brian P.
;      REGISTRATION NUMBER:  32,747
;      REFERENCE/DOCKET NUMBER:  18046.033
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-824-8000
;      TELEFAX:  202-824-8199
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-432-043-6

  Query Match             1.2%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 4.5e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
           || |||||||||| ||||| |||||
Db      30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


RESULT 12
US-08-660-963-6/c
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; Sequence 6, Application US/08660963
; Patent No. 5852187
;  GENERAL INFORMATION:
;    APPLICANT:  Thorner, Michael O.
;    APPLICANT:  Gaylinn, Bruce D.
;    APPLICANT:  Horikawa, Reiko
;    APPLICANT:  Lyons Jr., Charles E.
;    TITLE OF INVENTION:  MOLECULAR CLONING OF THE OVINE PITUITARY
;    TITLE OF INVENTION:  GROWTH HORMONE RELEASING HORMONE RECPTOR
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
;      STREET:  Metropolitan Square Building, Suite 800, 1450
;      STREET:  G. Street
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,963
;      FILING DATE:  12-JUN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  O'Shaughnessy, Brian P.
;      REGISTRATION NUMBER:  32,747
;      REFERENCE/DOCKET NUMBER:  18046.036
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-824-8000
;      TELEFAX:  202-824-8199
;      TELEX:  248516
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-660-963-6

  Query Match             1.2%;  Score 20.2;  DB 2;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 4.5e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     599 GGTGGCTGCCCTGCGCTGGGTCCAG 623
           || |||||||||| ||||| |||||
Db      30 GGAGGCTGCCCTGAGCTGGCTCCAG 6


RESULT 13
US-09-264-737-8/c
; Sequence 8, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:
;  APPLICANT: Feng, Paul C.C.
;  APPLICANT: Ruff, Thomas G.
;  TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
;  TITLE OF INVENTION: Expression of Esterase Enzymes
;  FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
;  CURRENT APPLICATION NUMBER: US/09/264,737A
;  CURRENT FILING DATE: 1999-03-09
;  EARLIER APPLICATION NUMBER: 60/077,377
;  EARLIER FILING DATE: 1998-03-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: thermal amplification sequence homologous to RLE3
;   OTHER INFORMATION: divergent region flanking sequence
US-09-264-737-8

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  Best Local Similarity   65.9%;  Pred. No. 6.8e+03;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

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Db      47 CAGTACCGCCTGGGCATCGGTGGCTTCGGTTTCAACATCGATGA 4


RESULT 14
US-08-907-598-4/c
; Sequence 4, Application US/08907598
; Patent No. 6139833
;  GENERAL INFORMATION:
;    APPLICANT:  Burgess, Rob
;    APPLICANT:  Friedrich, Glenn
;    APPLICANT:  Zambrowicz, Brian
;    APPLICANT:  Sands, Arthur
;    TITLE OF INVENTION:  TARGETED GENE DISCOVERY
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/907,598
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  8535-015-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 493-4935
;      TELEFAX:  (650) 493-5556
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-08-907-598-4

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  Best Local Similarity   70.3%;  Pred. No. 9.3e+03;
  Matches   26;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     695 TGTCTCTGTTCTTGTTTTGTCTCCATTGGCCAAGAAC 731
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Db      39 TGTGTGAGTTCCTGTTCTGACTCATTTGGTGATGAAC 3


RESULT 15
US-08-426-020-3/c
; Sequence 3, Application US/08426020
; Patent No. 5676952
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;  GENERAL INFORMATION:
;    APPLICANT:  AUDONNET, JEAN-CHRISTOPHE F
;    APPLICANT:  DARTEIL, RAPHAEL J
;    APPLICANT:  RIVIERE, MICHEL A
;    APPLICANT:  ZELNIK, VLADIMIR
;    APPLICANT:  ROSS, LOUIS J
;    TITLE OF INVENTION:  HERPESVIRUSES TRANSFORMED TO EXPRESS gD
;    TITLE OF INVENTION:  IN VITRO
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: . LARSON AND TAYLOR
;      STREET:  727 SOUTH 23RD STREET
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/426,020
;      FILING DATE:  09-APR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SARRO, THOMAS P
;      REGISTRATION NUMBER:  19,396
;      REFERENCE/DOCKET NUMBER:  XI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-920-7200
;      TELEFAX:  703-892-8428
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-426-020-3

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  Best Local Similarity   70.3%;  Pred. No. 1e+04;
  Matches   26;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

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Perfect score: 1728
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 504518

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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c	2	22.4	1.3	50	9	US-09-978-697-361	Sequence 361, App
c	3	22.4	1.3	50	9	US-09-978-192A-361	Sequence 361, App
c	4	22.4	1.3	50	9	US-09-999-832A-361	Sequence 361, App
c	5	22.4	1.3	50	9	US-09-978-189-361	Sequence 361, App
c	6	22.4	1.3	50	9	US-09-978-608A-361	Sequence 361, App
c	7	22.4	1.3	50	9	US-09-978-191A-361	Sequence 361, App
c	8	22.4	1.3	50	9	US-09-978-403A-361	Sequence 361, App
c	9	22.4	1.3	50	9	US-09-978-564A-361	Sequence 361, App
c	10	22.4	1.3	50	9	US-09-978-585A-361	Sequence 361, App
c	11	22.4	1.3	50	9	US-10-017-081A-361	Sequence 361, App
c	12	22.4	1.3	50	9	US-09-978-824-361	Sequence 361, App
c	13	22.4	1.3	50	9	US-09-981-915A-361	Sequence 361, App
c	14	22.4	1.3	50	9	US-09-999-833A-361	Sequence 361, App
c	15	22.4	1.3	50	9	US-10-167-749-361	Sequence 361, App
c	16	22.4	1.3	50	9	US-09-918-585A-361	Sequence 361, App
c	17	22.4	1.3	50	9	US-09-978-423A-361	Sequence 361, App
c	18	22.4	1.3	50	9	US-10-013-921A-361	Sequence 361, App
c	19	22.4	1.3	50	9	US-09-978-193A-361	Sequence 361, App
c	20	22.4	1.3	50	9	US-10-013-929A-361	Sequence 361, App
c	21	22.4	1.3	50	9	US-10-016-177A-361	Sequence 361, App
c	22	22.4	1.3	50	9	US-09-999-830A-361	Sequence 361, App
c	23	22.4	1.3	50	9	US-09-978-757A-361	Sequence 361, App
c	24	20.8	1.2	48	9	US-09-848-754A-8208	Sequence 8208, Ap
c	25	20.8	1.2	48	9	US-09-776-474-2832	Sequence 2832, Ap
c	26	20.6	1.2	35	10	US-09-731-393-3	Sequence 3, Appli
c	27	20.4	1.2	48	9	US-09-776-474-2738	Sequence 2738, Ap
	28	20.2	1.2	46	9	US-10-121-258-49	Sequence 49, Appl
c	29	20.2	1.2	46	9	US-10-121-258-50	Sequence 50, Appl
c	30	19.8	1.1	48	9	US-09-848-754A-8518	Sequence 8518, Ap
c	31	19.4	1.1	33	8	US-08-834-666A-26	Sequence 26, Appl
c	32	19.4	1.1	33	8	US-08-834-666A-29	Sequence 29, Appl
c	33	19.4	1.1	48	9	US-09-877-478-5309	Sequence 5309, Ap
c	34	19.4	1.1	48	9	US-09-848-754A-8732	Sequence 8732, Ap
	35	19.2	1.1	25	10	US-09-866-108-4102	Sequence 4102, Ap
	36	19.2	1.1	25	10	US-09-866-108-4103	Sequence 4103, Ap
c	37	19.2	1.1	31	9	US-09-773-599-4	Sequence 4, Appli
c	38	19.2	1.1	31	9	US-09-773-599-18	Sequence 18, Appl
c	39	19.2	1.1	43	10	US-09-944-411-27	Sequence 27, Appl
c	40	19.2	1.1	43	10	US-09-759-352-25	Sequence 25, Appl
c	41	19	1.1	36	10	US-09-731-393-4	Sequence 4, Appli
c	42	19	1.1	47	8	US-08-961-888-39	Sequence 39, Appl
c	43	19	1.1	48	9	US-09-780-164-2417	Sequence 2417, Ap
c	44	18.8	1.1	39	9	US-10-067-443-31	Sequence 31, Appl
c	45	18.8	1.1	48	9	US-09-780-164-2488	Sequence 2488, Ap

ALIGNMENTS

RESULT 1
US-09-978-295A-361/c
; Sequence 361, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 361, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
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; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 4
US-09-999-832A-361/c
; Sequence 361, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C63
;  CURRENT APPLICATION NUMBER: US/09/999,832A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
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;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
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;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/081817
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;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/081952
;  PRIOR FILING DATE: 1998-04-15
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;  PRIOR APPLICATION NUMBER: 60/082796
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; PRIOR FILING DATE: 1998-04-23
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; PRIOR APPLICATION NUMBER: 60/083495
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
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Db 50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3

RESULT 5
US-09-978-189-361/c
; Sequence 361, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-26
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; PRIOR FILING DATE: 1998-03-30
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; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
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Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 6
US-09-978-608A-361/c
; Sequence 361, Application US/09978608A
; Publication No. US20030045462A1

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 361
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-608A-361

  Query Match             1.3%;  Score 22.4;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
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RESULT 7
US-09-978-191A-361/c
; Sequence 361, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
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;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
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;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
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;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
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;  PRIOR FILING DATE: 1998-03-27
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;  PRIOR FILING DATE: 1998-03-27
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;  PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 8
US-09-978-403A-361/c
; Sequence 361, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 9
US-09-978-564A-361/c
; Sequence 361, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
          || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 10
US-09-978-585A-361/c
; Sequence 361, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 361
; LENGTH: 50
; TYPE: DNA

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-585A-361

  Query Match             1.3%;  Score 22.4;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
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Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


RESULT 11
US-10-017-081A-361/c
; Sequence 361, Application US/10017081A
; Publication No. US20030049684A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C69
;  CURRENT APPLICATION NUMBER: US/10/017,081A
;  CURRENT FILING DATE:  2002-04-30
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 361
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-081A-361

  Query Match             1.3%;  Score 22.4;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
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Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


RESULT 12
US-09-978-824-361/c
; Sequence 361, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C14
;  CURRENT APPLICATION NUMBER: US/09/978,824
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
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;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078936
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079664
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;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
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; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
          || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 13
US-09-981-915A-361/c
; Sequence 361, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
          || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 14
US-09-999-833A-361/c
; Sequence 361, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
          || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3
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RESULT 15
US-10-167-749-361/c
; Sequence 361, Application US/10167749
; Publication No. US20030056137A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

```
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C60
;  CURRENT APPLICATION NUMBER: US/10/167,749
;  CURRENT FILING DATE:  2001-10-19
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
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;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 361
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-167-749-361

  Query Match             1.3%;  Score 22.4;  DB 9;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+03;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1209 GAAGCCACTGAGAAATACTTAGGAGGAACAGACGACACTGTCAAAAAG 1256
          || || |||||| |||   |  |||| || | | ||  || |||| ||
Db     50 GAGGCGACTGAGGAATGGGTTAGAGGTACTGGCAACGTTGACAAAGAG 3


Search completed: May 21, 2003, 06:31:28
Job time : 902 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:12:59 ; Search time 2271 Seconds
(without alignments)
12323.118 Million cell updates/sec

Title: US-09-920-394-3_COPY_14_1741
Perfect score: 1728
Sequence: 1 tgtcgcccttcacgatgtgg.....catagagctgtgaatgaaga 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21.8	1.3	43	9	AA472672	AA472672 vh04g03.r
	2	20.8	1.2	50	17	AZ386495	AZ386495 1M0145E01
	3	20.6	1.2	50	17	AZ785734	AZ785734 2M0029I24
	4	20.4	1.2	49	9	AI348359	AI348359 qo20f09.x
	5	20.2	1.2	36	17	AZ491747	AZ491747 1M0325D04
c	6	20.2	1.2	43	17	AZ391814	AZ391814 1M0154H11
	7	20.2	1.2	49	9	AA627247	AA627247 nq64d09.s
c	8	20	1.2	49	10	AW246898	AW246898 2822473.5
	9	20	1.2	50	9	AU105489	AU105489 AU105489
	10	20	1.2	50	9	AU105492	AU105492 AU105492
c	11	19.8	1.1	50	9	AU106827	AU106827 AU106827
	12	19.6	1.1	49	9	AA013617	AA013617 mh10d05.r
	13	19.6	1.1	49	9	AA894674	AA894674 oj27a03.s
	14	19.6	1.1	50	9	AU105977	AU105977 AU105977
	15	19.6	1.1	50	9	AU107832	AU107832 AU107832
	16	19.6	1.1	50	14	C01080	C01080 HUMGS000773
	17	19.6	1.1	50	17	AG024509	AG024509 Oryza sat
	18	19.4	1.1	40	17	AZ491349	AZ491349 1M0324C22
	19	19.4	1.1	48	17	BH896737	BH896737 3526_1_5_
c	20	19.4	1.1	49	9	AI687542	AI687542 tp88g04.x
	21	19.2	1.1	34	14	H41313	H41313 yp68g05.s1
c	22	19.2	1.1	37	12	BF211603	BF211603 601812103
	23	19.2	1.1	47	17	BH864137	BH864137 SALK_0954
	24	19.2	1.1	50	9	AU102327	AU102327 AU102327
c	25	19.2	1.1	50	9	AU105236	AU105236 AU105236
	26	19	1.1	41	17	AZ630226	AZ630226 1M0483L11
c	27	19	1.1	42	17	AL756150	AL756150 Arabidops
	28	19	1.1	50	9	AU102282	AU102282 AU102282
	29	19	1.1	50	9	AU105218	AU105218 AU105218
	30	18.8	1.1	45	13	BI102544	BI102544 602889548
c	31	18.8	1.1	48	12	BF032107	BF032107 601559702
c	32	18.8	1.1	48	17	AZ510557	AZ510557 1M0355E12
	33	18.8	1.1	50	9	AU102668	AU102668 AU102668
	34	18.6	1.1	46	14	BQ704909	BQ704909 Bn01_01c2
	35	18.6	1.1	49	12	BF722018	BF722018 mab27b06.
	36	18.6	1.1	50	9	AU104828	AU104828 AU104828
	37	18.6	1.1	50	9	AU107833	AU107833 AU107833
	38	18.4	1.1	38	17	AZ506007	AZ506007 1M0346P19
	39	18.4	1.1	40	17	TA115C11P	AL462827 T. brucei
c	40	18.4	1.1	41	17	AZ463683	AZ463683 1M0272L09
	41	18.4	1.1	42	17	AZ401452	AZ401452 1M0168K04
	42	18.4	1.1	44	17	BH000259	BH000259 2M0288A03
c	43	18.4	1.1	45	12	BE738342	BE738342 601572726
c	44	18.4	1.1	46	9	AI784970	AI784970 uj22d02.x
	45	18.4	1.1	50	9	AU106899	AU106899 AU106899

ALIGNMENTS

RESULT 1
AA472672
LOCUS AA472672 43 bp mRNA linear EST 18-JUN-1997
DEFINITION vh04g03.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:874516 5' similar to SW:NUPM_BOVIN P42029 NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT ;, mRNA sequence.
ACCESSION AA472672
VERSION AA472672.1 GI:2200954
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:513996
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:874516"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 11 a 8 c 17 g 7 t
ORIGIN

Query Match 1.3%; Score 21.8; DB 9; Length 43;
Best Local Similarity 70.7%; Pred. No. 1e+05;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy    990 GGGATGCTGCTGCTGAAAACACCTGAAGAGCTTCAAGCTGA 1030
          ||||| || |||| ||| | |||||||| |||| ||
Db      2 GGGATAGTGGAGCTGCCAACTCTGGAAGAGCTGCAAGTCGA 42
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RESULT 2
AZ386495
LOCUS AZ386495 50 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0145E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0145E01 R, DNA sequence.
ACCESSION AZ386495
VERSION AZ386495.1 GI:10500195
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: E column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145E01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 10 c 13 g 11 t
ORIGIN

Query Match 1.2%; Score 20.8; DB 17; Length 50;
Best Local Similarity 70.0%; Pred. No. 2.3e+05;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy   1652 TTTCTGGACCAACCTCTTTGCCAAGAAGGCAGTGGAGAAG 1691
          || ||| || ||| || | |||||||| ||| | | ||
Db      9 TTCCTGCACAAACATCATGACCAAGAAGCAAGTTGGGGAG 48
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RESULT 3
AZ785734
LOCUS AZ785734 50 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0029I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0029I24 R, DNA sequence.
ACCESSION AZ785734
VERSION AZ785734.1 GI:12922790
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: I column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.

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FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0029I24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a      9 c     16 g     13 t
ORIGIN

  Query Match             1.2%;  Score 20.6;  DB 17;  Length 50;
  Best Local Similarity   67.4%;  Pred. No. 2.7e+05;
  Matches   29;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     598 AGGTGGCTGCCCTGCGCTGGGTCCAGGACAACATTGCCAGCTT 640
           | ||||      || ||||||| ||||| | ||||||   |||
Db       7 AAGTGGAGAATGTGAGCTGGGTGCAGGAAATCATTGCTCCCTT 49


RESULT 4
AI348359
LOCUS       AI348359                 49 bp    mRNA    linear   EST 01-FEB-1999
DEFINITION  qo20f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1909097 3'
            similar to SW:NMA_HUMAN Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA
            PRECURSOR. ;, mRNA sequence.
ACCESSION   AI348359
VERSION     AI348359.1  GI:4085565
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 696   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
```

```
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1909097"
                     /clone_lib="NCI_CGAP_Lu5"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       11 a     13 c     12 g     13 t
ORIGIN

  Query Match             1.2%;  Score 20.4;  DB 9;  Length 49;
  Best Local Similarity   71.1%;  Pred. No. 3e+05;
  Matches   27;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    1315 TGGCCCGGAACCACAGAGATGCTGGAGCACCCACCTAC 1352
           |||||||||||||||    |  ||||| |   | ||||
Db       1 TGGCCCGGAACCACAACTCTTTTGGAGAAGTTAGCTAC 38


RESULT 5
AZ491747
LOCUS       AZ491747                 36 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0325D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0325D04 R, DNA sequence.
ACCESSION   AZ491747
VERSION     AZ491747.1  GI:10663751
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0325  row: D  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0325D04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 7 c 14 g 6 t
ORIGIN

Query Match 1.2%; Score 20.2; DB 17; Length 36;
Best Local Similarity 75.8%; Pred. No. 2.9e+05;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 873 CTGCGACAGAAGACGGAAGAGGAGCTCTTGGAG 905
||| |||| | |||| || || ||||||||||
Db 1 CTGGGACACCAAACGGGGGATGATCTCTTGGAG 33

RESULT 6
AZ391814/c
LOCUS AZ391814 43 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0154H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0154H11 F, DNA sequence.
ACCESSION AZ391814
VERSION AZ391814.1 GI:10506886
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0154 row: H column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0154H11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 8 c 7 g 15 t
ORIGIN

Query Match 1.2%; Score 20.2; DB 17; Length 43;
Best Local Similarity 75.8%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1624 CCCAGAAGCTGAAGGACAAAGAAGTAGCTTTCT 1656
||||||| ||| | ||||||| |||||| |
Db 38 CCCAGAAACTGGACTGCAAAGAATGAGCTTTAT 6

RESULT 7
AA627247
LOCUS AA627247 49 bp mRNA linear EST 31-OCT-1997
DEFINITION nq64d09.s1 NCI_CGAP_Ov6 Homo sapiens cDNA clone IMAGE:1154801 similar to TR:G1144330 G1144330 CREB-RP. ;, mRNA sequence.
ACCESSION AA627247
VERSION AA627247.1 GI:2540291
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Andrew Berchuck, M.D., Elise Kohn, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 423 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1154801"
/clone_lib="NCI_CGAP_Ov6"
/sex="female"
/tissue_type="normal cortical stroma"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP10; mRNA made from normal ovarian cortical stroma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. "

```
BASE COUNT       13 a      8 c     22 g      6 t
ORIGIN

  Query Match             1.2%;  Score 20.2;  DB 9;  Length 49;
  Best Local Similarity   68.3%;  Pred. No. 3.5e+05;
  Matches   28;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    452 GGTGGGTGCGGCATCAACCTATGATGGGCTGGCCCTTGCTG 492
          || || || || | | |    ||| ||||||||||| || |
Db      4 GGAGGTTGAGGAAGCGAAGACTGAGGGGCTGGCCCTAGCAG 44


RESULT 8
AW246898/c
LOCUS       AW246898                 49 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822473 5',
            mRNA sequence.
ACCESSION   AW246898
VERSION     AW246898.1  GI:6589891
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822473.3prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 19
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 49 contiguous distinct
            peaks following vector sequence. Short Insert: Based upon the
            presence of vector at both ends of the untrimmed sequence, this
            clone probably contains a cDNA insert of approximately 464 bases.
            Plate: LLCM9  row: I  column: 2
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822473"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT       21 a      6 c     18 g      4 t
ORIGIN

  Query Match             1.2%;  Score 20;  DB 10;  Length 49;
  Best Local Similarity   65.9%;  Pred. No. 4.1e+05;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    703 TTCTTGTTTTGTCTCCATTGGCCAAGAACCTCTTCCACCGGGCC 746
          || || ||||| | || ||  ||| | | | |||| || |||
Db     44 TTTTTTTTTGCCCCCCTTCACCACAAGCTTTTCCCTCGTGCC 1


RESULT 9
AU105489
LOCUS       AU105489                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105489 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            COLF0946, mRNA sequence.
ACCESSION   AU105489
VERSION     AU105489.1  GI:13555010
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="COLF0946"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT       15 a      11 c     17 g      7 t
ORIGIN

  Query Match             1.2%;  Score 20;  DB 9;  Length 50;
  Best Local Similarity   65.9%;  Pred. No. 4.1e+05;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    557 AGGGGATGAACACAGCCGGGGGAACTGGGGTCACCTGGACCAGG 600
          || ||||  | ||  |  || | ||| ||  |||||| | ||||
Db      1 AGAGGATCCAGACGCCTTGGAGGACTTGGAGCACCTGTAACAGG 44


RESULT 10
AU105492
LOCUS       AU105492                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105492 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC12761, mRNA sequence.
ACCESSION   AU105492
VERSION     AU105492.1  GI:13555013
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
```

```
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="HRC12761"
                      /clone_lib="Sugano Homo sapiens cDNA library"
                      /note="Differential display comparison of untreated and
                      dimethylfumarate treated U937 cells"
BASE COUNT       16 a     11 c     16 g      7 t
ORIGIN

  Query Match             1.2%;  Score 20;  DB 9;  Length 50;
  Best Local Similarity   65.9%;  Pred. No. 4.1e+05;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     557 AGGGGATGAACACAGCCGGGGGAACTGGGGTCACCTGGACCAGG 600
           || ||||  | ||  |  || | ||| ||  |||||| | ||||
Db       1 AGAGGATCCAGACGCCTTGGAGGACTTGGAACACCTGTAACAGG 44


RESULT 11
AU106827/c
LOCUS       AU106827                  50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU106827 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP20988, mRNA sequence.
ACCESSION   AU106827
VERSION     AU106827.1  GI:13556348
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="HEP20988"
                      /clone_lib="Sugano Homo sapiens cDNA library"
                      /note="Differential display comparison of untreated and
                      dimethylfumarate treated U937 cells"
BASE COUNT       11 a     14 c     14 g     11 t
ORIGIN

  Query Match             1.1%;  Score 19.8;  DB 9;  Length 50;
  Best Local Similarity   69.2%;  Pred. No. 4.8e+05;
  Matches   27;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    1593 TATCTGCAGATTGGTGCCAACACCCAGGCGGCCCAGAAG 1631
           | |||  ||| |||||||||| ||   ||| | |  |||

Db      41 TTTCTAGAGACTGGTGCCAACGCCGTAGCGCCGCGAAAG 3


RESULT 12
AA013617
LOCUS       AA013617                  49 bp    mRNA    linear   EST 21-JAN-1997
DEFINITION  mh10d05.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
            clone IMAGE:442089 5' similar to WP:F35G12.9 CE00978 ;, mRNA
            sequence.
ACCESSION   AA013617
VERSION     AA013617.1  GI:1474645
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:267425
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: ETPrimer
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .49
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:442089"
                      /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                      /sex="unknown"
                      /tissue_type="placenta"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                      with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      1st strand cDNA was primed with a Not I - oligo(dT) primer
                      [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization, and was
                      constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT        7 a     13 c     15 g     14 t
ORIGIN

  Query Match             1.1%;  Score 19.6;  DB 9;  Length 49;
  Best Local Similarity   66.7%;  Pred. No. 5.4e+05;
  Matches   28;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     605 TGCCCTGCGCTGGGTCCAGGACAACATTGCCAGCTTTGGAGG 646
           |||| |  || |||||||||  |    |||| || || || |
Db       7 TGCCATCTGCAGGGTCCAGGTGATGGATGCCTGCCTTCGATG 48


RESULT 13
AA894674
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LOCUS       AA894674                 49 bp    mRNA    linear   EST 09-JUN-1998
DEFINITION  oj27a03.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1493356 3'
            similar to SW:SPCO_HUMAN Q01082 SPECTRIN BETA CHAIN, BRAIN ;, mRNA
            sequence.
ACCESSION   AA894674
VERSION     AA894674.1  GI:3031075
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1272   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .49
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1493356"
                      /clone_lib="NCI_CGAP_Kid3"
                      /lab_host="DH10B"
                      /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer,
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not
                      I and Eco RI sites  of the modified pT7T3 vector.  mRNA
                      source: 2 pooled kidneys. Library went through one round
                      of normalization. Library constructed by Bento Soares and
                      M. Fatima Bonaldo.  "
BASE COUNT       13 a     13 c     16 g      7 t
ORIGIN

  Query Match             1.1%;  Score 19.6;  DB 9;  Length 49;
  Best Local Similarity   66.7%;  Pred. No. 5.4e+05;
  Matches   28;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     572 CCGGGGGAACTGGGGTCACCTGGACCAGGTGGCTGCCCTGCG 613
           ||||| | | |||||  |||| || ||| |    ||| | ||
Db       1 CCGGGAGCAGTGGGGCAACCTAGAACAGCTCTTCGCCATTCG 42


RESULT 14
AU105977
LOCUS       AU105977                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU105977 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ISMA0065, mRNA sequence.
ACCESSION   AU105977
VERSION     AU105977.1  GI:13555498
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
     source           1. .50
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                      /clone="ISMA0065"
                      /clone_lib="Sugano Homo sapiens cDNA library"
                      /note="Differential display comparison of untreated and
                      dimethylfumarate treated U937 cells"
BASE COUNT       10 a     17 c     11 g     12 t
ORIGIN

  Query Match             1.1%;  Score 19.6;  DB 9;  Length 50;
  Best Local Similarity   73.5%;  Pred. No. 5.5e+05;
  Matches   25;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy     868 ACTGCCTGCGACAGAAGACGGAAGAGGAGCTCTT 901
           ||| |||||||| | |||    ||||  ||||||
Db       4 ACTCCCTGCGACTGCAGAACTCAGAGCTGCTCTT 37


RESULT 15
AU107832
LOCUS       AU107832                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU107832 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV61059, mRNA sequence.
ACCESSION   AU107832
VERSION     AU107832.1  GI:13557354
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES              Location/Qualifiers
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                     /clone="ZRV61059"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        4 a     18 c     20 g      7 t      1 others
ORIGIN

  Query Match             1.1%;  Score 19.6;  DB 9;  Length 50;
  Best Local Similarity   71.4%;  Pred. No. 5.5e+05;
  Matches   25;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    433 TCCACGGAGGGGGGCTGATGGTGGGTGCGGCATCA 467
          ||| |||  |   ||||  ||| ||||||||  |||
Db      3 TCCCCGGCTGANCGCTGGCGGTCGGTGCGGCGTCA 37


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Job time : 2276 secs
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